Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix `BLOSUM62 ▼` gap open: `11` gap extension: `1`
x_dropoff: `0` expect: `10.000` wordsize: `3` Filter `☐` View option `Standard ▼`
Masking character option `X for protein, n for nucleotide ▼` Masking color option `Black ▼`
`☐` Show CDS translation `Align`

Sequence 1: results for sequence "sin2" starting "AspIleValMet"
Length = 108 (1 .. 108)

Sequence 2: results for sequence "sin4" starting "AspIleLeuMet"
Length = 108 (1 .. 108)
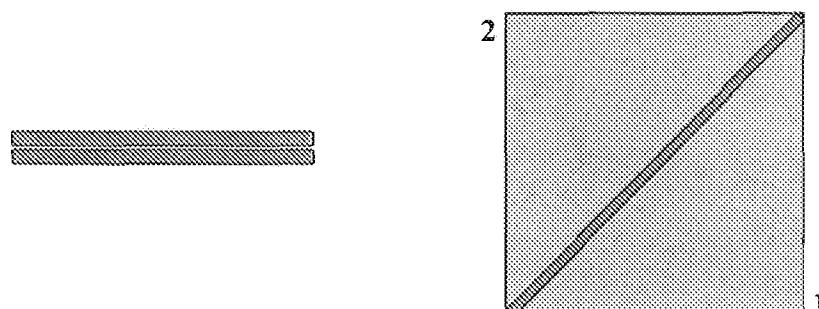
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  178 bits (452),  Expect = 9e-44
 Identities = 86/108 (79%), Positives = 96/108 (88%), Gaps = 0/108 (0%)
                                CDR-1                        CDR-2
Query  1    DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPA  60
            DI+MTQS KFMSTSVGDRVS+TCKASQ+V   VAWYQQKPGQSPK LIYSASYRY+GVP
Sbjct  1    DILMTQSQKFMSTSVGDRVSVTCKASQNVGINVAWYQQKPGQSPKALIYSASYRYSGVPD  60

Query  61   RFSGSGSGTDFTFTISSVQTEDLAVYYCQQHYRTPPTFGGGTKLELKR  108
            RF+GSGSGTDFT TIS+VQ+EDLA Y+CQQ+   P TFGGGTKLE+KR
Sbjct  61   RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGGGTKLEIKR  108
                                       CDR-3
```

```
CPU time:     0.05 user secs.      0.03 sys. secs      0.08 total secs.
```

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Matrix [BLOSUM62 ▾] gap open: [11] gap extension: [1]

x_dropoff: [0] expect: [10.0000] wordsize: [3] Filter ☐ View option [Standard ▾]

Masking character option [X for protein, n for nucleotide ▾] Masking color option [Black ▾]

☐ Show CDS translation [Align]

Sequence 1: results for sequence "sin1" starting "GlnValGlnLeu"
Length = 120 (1 .. 120)

Sequence 2: results for sequence "sin3" starting "GlnValGlnLeu"
Length = 119 (1 .. 119)
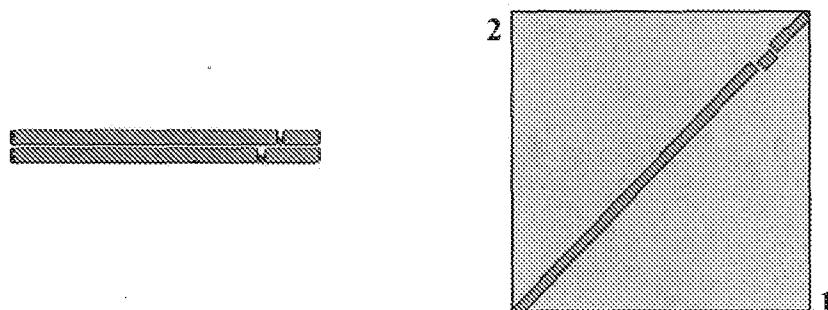
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  157 bits (396),  Expect = 3e-37
 Identities = 79/122 (64%),  Positives = 94/122 (77%), Gaps = 5/122 (4%)
                                        CDR1              CDR2
Query  1    QVQLKQSGAELVRPGASVRLSCKASGYTFTYYWINWIKQRPEQGLEWIGRIDPYDSETRY  60
            QVQL+QSG EL +PGASV++SCKASGY+F+ Y +N W+KQ   + LEWIG IDPY+ +T Y
Sbjct  1    QVQLQQSGPELEKPGASVKISCKASGYSFSDYNMNWVKQSNGKSLEWIGNIDPYNGDTNY  60

                                                          CDR3
Query  61   NQKFKDKAILTVDKYSSTAYMQLSSLTSEDSAVYYCAKGVYDGHWF--FDVWGAGTSVTV  118
            NQKFK KA LT+DK SSTAYMQL SLTSEDSAVY+CA+      W   F  WG GT VTV
Sbjct  61   NQKFKGKATLTLDKSSSTAYMQLKSLTSEDSAVYFCAR--SRGWLLPFAYWGQGTLVTV  117

Query  119  SS  120
            S+
Sbjct  118  SA  119


CPU time:      0.04 user secs.       0.04 sys. secs       0.08 total secs.
```

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 ▾ gap open: 11 gap extension: 1
x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☐ View option Standard ▾
Masking character option X for protein, n for nucleotide ▾ Masking color option Black ▾
☐ Show CDS translation Align

Sequence 1: results for sequence "sin7" starting "GlnValGlnLeu"
Length = 119 (1 .. 119)

Sequence 2: results for sequence "sin25" starting "GluValGlnLeu"
Length = 117 (1 .. 117)
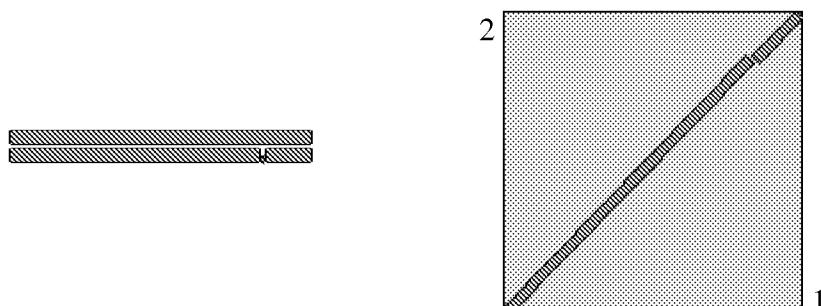
NOTE: Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  159 bits (402),  Expect = 6e-38
 Identities = 77/119 (64%), Positives = 95/119 (79%), Gaps = 2/119 (1%)

Query   1    QVQLQQSGGELVRPGTSVKVSCKASGYAFTNYLIEWIRQRPGQGLEWIGVINPGSGNSKS   60
             +VQLQQSG ELVRPG SVK+SCK S Y FT+Y + W++Q   + LEWIGVI+   GN K
Sbjct   1    EVQLQQSGPELVRPGVSVKISCKGSSYKFTDYAMHWVKQSHAKSLEWIGVISTYYGNVKY   60

Query   61   SKNLKGKATLTADKSSNTAYMQLSSLTSDDSAVYFCARSGVYGSSPDYWGQGTTLTVSS   119
             ++  KGKAT+T DKSS+TAYM+L+ LTS+DSAVY+CARS  YGS  DYWGQGT++TVSS
Sbjct   61   NQKFKGKATMTVDKSSSTAYMELARLTSEDSAVYYCARS--YGSYLDYWGQGTSVTVSS   117


CPU time:     0.04 user secs.      0.04 sys. secs      0.08 total secs.
```

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 ▾ gap open: 11   gap extension: 1
x_dropoff: 0   expect: 10.0000 wordsize: 3   Filter ☐ View option Standard ▾
Masking character option X for protein, n for nucleotide ▾   Masking color option Black ▾
☐ Show CDS translation   Align

Sequence 1: results for sequence "sin8" starting "AspValValMet"
Length = 113 (1 .. 113)

Sequence 2: results for sequence "sin26" starting "AspIleValMet"
Length = 112 (1 .. 112)
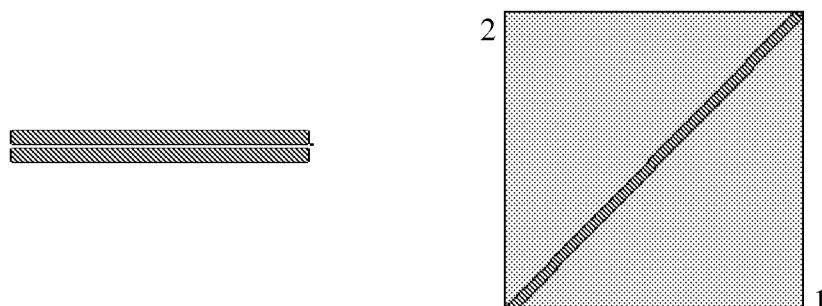
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  227 bits (579),  Expect = 2e-58
 Identities = 110/112 (98%), Positives = 111/112 (99%), Gaps = 0/112 (0%)

Query  1     DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD   60
             D+VMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD
Sbjct  1     DIVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD   60

Query  61    SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIK   112
             SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP TFGGGTKLEIK
Sbjct  61    SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPWTFGGGTKLEIK   112


CPU time:     0.05 user secs.       0.03 sys. secs        0.08 total secs.
```